CRF Errors Corrected by the STIC Systems Branch

1600
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MAR 24 2003
TECH CENTER 1600/2900

CRF Processing Date: 3/24/2003
Edited by:
Verified by: (STIC Staff)

Serial Number: 09/607,745 ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: Sequence 9 - aligned amino acid number

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING DATE: 03/18/2003
PATENT APPLICATION: **US/09/607,745** TIME: 18:41:22

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\03182003\I607745.raw**

3 <110> APPLICANT: Darrow, Andrew L
4 Qi, Jain-shen
5 Andrade-Gordon, Patricia
7 <120> TITLE OF INVENTION: DNA encoding human serine protease D-G
9 <130> FILE REFERENCE: ORT-1273
C--> 11 **<140> CURRENT APPLICATION NUMBER: US/09/607,745**
C--> 12 **<141> CURRENT FILING DATE: 2000-06-30**
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2121
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <400> SEQUENCE: 1
24 caacttcact tgtagggctg ttttaatcaa gctgcccaaa gtcccccaat cactcctgga 60
25 atacacagag agaggcagca gcttgctcag cggacaagga tgctgggcgt gagggaccaa 120
26 ggcctgccct gcactcgggc ctcctccagc cagtgctgac cagggacttc tgacctgctg 180
27 gccagccagg acctgtgtgg ggaggccctc ctgctgcctt ggggtgacaa tctcagctcc 240
28 aggctacagg gagaccggga ggatcacaga gccagcatgg atcctgacag tgatcaacct 300
29 ctgaacagcc tcgatgtcaa acccctgcgc aaaccccgta tccccatgga gaccttcaga 360
30 aaggtgggga tccccatcat catagcacta ctgagcctgg cgagtatcat cattgtggtt 420
31 gtcctcatca aggtgattct ggataaatac tacttcctct gcgggcagcc tctccacttc 480
32 atcccgagga agcagctgtg tgacggagag ctggactgtc ccttggggga ggacgaggag 540
33 cactgtgtca agagcttccc cgaagggcct gcagtggcag tccgcctctc caaggaccga 600
34 tccacactgc aggtgctgga ctcggccaca gggaactggt tctctgcctg tttcgacaac 660
35 ttcacagaag ctctcgctga gacagcctgt aggcagatgg gctacagcag caaacccact 720
36 ttcagagctg tggagattgg cccagaccag gatctggatg ttgttgaaat cacagaaaac 780
37 agccaggagc ttcgcatgcg gaactcaagt gggccctgtc tctcaggctc cctggtctcc 840
38 ctgcactgtc ttgcctgtgg gaagagcctg aagacccccc gtgtggtggg tggggaggag 900
39 gcctctgtgg attcttggcc ttggcaggtc agcatccagt acgacaaaca gcacgtctgt 960
40 ggagggagca tcctggaccc ccactgggtc ctcacggcag cccactgctt caggaaacat 1020
41 accgatgtgt tcaactggaa ggtgcgggca ggctcagaca aactgggcag cttcccatcc 1080
42 ctggctgtgg ccaagatcat catcattgaa ttcaacccca tgtaccccaa agacaatgac 1140
43 atcgccctca tgaagctgca gttcccactc actttctcag gcacagtcag gcccatctgt 1200
44 ctgcccttct ttgatgagga gctcactcca gccaccccac tctggatcat tggatggggc 1260
45 tttacgaagc agaatggagg gaagatgtct gacatactgc tgcaggcgtc agtccaggtc 1320
46 attgacagca cacggtgcaa tgcagacgat gcgtacctgg gggaagtcac cgagaagatg 1380
47 atgtgtgcag gcatcccgga agggggtgtg gacacctgcc agggtgacag tggtgggccc 1440
48 ctgatgtacc aatctgacca gtggcatgtg gtgggcatcg ttagctgggg ctatggctgc 1500
49 gggggcccga gcaccccagg ggtatacacc aaggtctcag cctatctcaa ctggatctac 1560
50 aatgtctgga aggctgagct gtaatgctgc tgccccttg cagtgctggg agccgcttcc 1620
51 ttcctgccct gcccacctgg ggatccccca aagtcagaca cagagcaaga gtccccttgg 1680
52 gtacacccct ctgcccacag cctcagcatt tcttggagca gcaaagggcc tcaattccta 1740

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taagagaccc tcgcagccca gaggcgccca gaggaagtca gcagccctag ctcggccaca 1800
cttggtgctc ccagcatccc agggagagac acagcccact gaacaaggtc tcaggggtat 1860
tgctaagcca agaaggaact ttcccacact actgaatgga agcaggctgt cttgtaaaag 1920
cccagatcac tgtgggctgg agaggagaag gaaagggtct gcgccagccc tgtccgtctt 1980
cacccatccc caagcctact agagcaagaa accagttgta atataaaatg cactgcctac 2040
tgttggtatg actaccgtta cctactgttg tcattgttat tacagctatg gccactatta 2100
ttaaagagct gtgtaacatc a 2121

<210> SEQ ID NO: 2
<211> LENGTH: 435
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

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 1               5                  10                  15
Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val Gly Ile
            20                  25                  30
Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile Val Val
        35                  40                  45
Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys Gly Gln
    50                  55                  60
Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu Leu Asp
65                  70                  75                  80
Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe Pro Glu
                85                  90                  95
Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr Leu Gln
            100                 105                 110
Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn
        115                 120                 125
Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser
    130                 135                 140
Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln Asp Leu
145                 150                 155                 160
Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met Arg Asn
                165                 170                 175
Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His Cys Leu
            180                 185                 190
Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly Glu Glu
        195                 200                 205
Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys
    210                 215                 220
Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr
225                 230                 235                 240
Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val
                245                 250                 255
Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala
            260                 265                 270
Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
        275                 280                 285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr Val
```

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Input Set : A:\PTO.AMC.txt
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```
123     290                 295                 300
125 Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro Ala Thr
126 305                 310                 315                 320
128 Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly Gly Lys
129                 325                 330                 335
131 Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp Ser Thr
132             340                 345                 350
134 Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu Lys Met
135         355                 360                 365
137 Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln Gly Asp
138     370                 375                 380
140 Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val Val Gly
141 385                 390                 395                 400
143 Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro Gly Val
144                 405                 410                 415
146 Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val Trp Lys
147             420                 425                 430
149 Ala Glu Leu
150         435
153 <210> SEQ ID NO: 3
154 <211> LENGTH: 20
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
160       oligonucleotide primer
162 <400> SEQUENCE: 3
163 acagcctcag catttcttgg                                              20
166 <210> SEQ ID NO: 4
167 <211> LENGTH: 20
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
173       oligonucleotide primer
175 <400> SEQUENCE: 4
176 tcttgctcta gtaggcttgg                                              20
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 40
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: Nested probe
187 <400> SEQUENCE: 5
188 ttggtgctcc cagcatccca gggagagaca cagcccactg                        40
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 30
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING DATE: 03/18/2003
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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\03182003\I607745.raw

<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonucleotide primer
<400> SEQUENCE: 6
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<210> SEQ ID NO: 7
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonucleotide primer
<400> SEQUENCE: 7
gatgtctaga cagctcagcc ttccagacat tg 32
<210> SEQ ID NO: 8
<211> LENGTH: 1189
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
<400> SEQUENCE: 8
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gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120
gtggacgcgg ccgctcttgc tgccccctttt gatgatgatg acaagatcgt tgggggctat 180
gctctagatg tggattcttg gccttggcag gtcagcatcc agtacgacaa acagcacgtc 240
tgtggaggga gcatcctgga cccccactgg gtcctcacgg cagcccactg cttcaggaaa 300
cataccgatg tgttcaactg gaaggtgcgg gcaggctcag acaaactggg cagcttccca 360
tccctggctg tggccaagat catcatcatt gaattcaacc ccatgtaccc caaagacaat 420
gacatcgccc tcatgaagct gcagttccca ctcactttct caggcacagt caggcccatc 480
tgtctgccct tctttgatga ggagctcact ccagccaccc cactctggat cattggatgg 540
ggctttacga agcagaatgg agggaagatg tctgacatac tgctgcaggc gtcagtccag 600
gtcattgaca gcacacggtg caatgcagac gatgcgtacc tgggggaagt caccgagaag 660
atgatgtgtg caggcatccc ggaaggggtg gtggacacct gccagggtga cagtggtggg 720
cccctgatgt accaatctga ccagtggcat gtggtgggca tcgttagctg gggctatggc 780
tgcgggggcc cgagcacccc aggggtatac accaaggtct cagcctatct caactggatc 840
tacaatgtct ggaaggctga gctgtctaga catcaccatc accatcacta gcggccgctt 900
ccctttagtg agggttaatg cttcgagcag acatgataag atacattgat gagtttggac 960
aaaccacaac tagaatgcag tgaaaaaaat gctttatttg tgaaatttgt gatgctattg 1020
ctttatttgt aaccattata agctgcaata aacaagttag cttgtcgaga agtactagag 1080
gatcataatc agccatacca catttgtaga ggttttactt gctttaaaaa acctcccaca 1140
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<210> SEQ ID NO: 9
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
<400> SEQUENCE: 9
Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu

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```
258   1               5                  10                  15
260 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
261             20                  25                  30
263 Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp
264         35                  40                  45
266 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Asp Val Asp Ser Trp Pro
267     50                  55                  60
269 Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser
270 65                  70                  75                  80
272 Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys
273                 85                  90                  95
275 His Thr Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu
276             100                 105                 110
278 Gly Ser Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe
279         115                 120                 125
281 Asn Pro Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln
282     130                 135                 140
284 Phe Pro Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe
285 145                 150                 155                 160
287 Phe Asp Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp
288                 165                 170                 175
290 Gly Phe Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln
291             180                 185                 190
293 Ala Ser Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala
294         195                 200                 205
296 Tyr Gln Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu
297     210                 215                 220
299 Gly Gly Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr
300 225                 230                 235                 240
302 Gln Ser Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly
303                 245                 250                 255
305 Cys Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
306             260                 265                 270
308 Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu Ser Arg His His
309         275                 280                 285
311 His His His His
312     290
```

VERIFICATION SUMMARY DATE: 03/18/2003
PATENT APPLICATION: US/09/607,745 TIME: 18:41:23

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\03182003\I607745.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date